

**AMENDMENTS TO THE SPECIFICATION:**

Please amend the paragraph beginning at page 7, line 2, as follows:

Fig. 5 Figs. 5A-1 to 5A-39. Sequences corresponding to GenBank Accession Nos. shown in Table III.

Please amend the paragraph beginning at page 9, line 9, as follows:

One of the major advantages in using *C. elegans* as a model system, for example, to identify new metal-responsive genes, is the magnitude of cDNA and genomic DNA sequence data currently available. The nematode genome is relatively small ( $\sim 10^8$  bp), and an abundance of information is available on the genetic and physical maps of its chromosomes (Waterston, R.H. et al. in *C. elegans II* (Riddle, D.L., Blumenthal, T., Meyer, B.J. and Priess, J.R., eds) pp. 23-46, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Currently, sequencing of the entire *C. elegans* genome is >80% completed and >50,000 ESTs have been cloned and sequenced. Megabases of genomic and cDNA sequence data are readily available through GenBank, the *C. elegans* Genome Project (Coulson, A. (1996) *Biochem. Soc. Trans.* 24, 289-291) and the *C. elegans* cDNA Sequencing Project (Sequence data and information about the *C. elegans* DNA Project can be obtained at [http://www.ddbj.nig.ac.jp/c-elegans/html/CE\\_INDEX.html](http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) / http colon forward slash forward slash www dot ddbj dot nig dot ac dot jp forward slash c hyphen elegans forward slash html forward slash CE underscore INDEXZ dot html forward slash).